

Appl. No. : 09/344,526
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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

LISTING OF CLAIMS

1-15. (Cancelled)

16. (Previously presented) A method of making a microsphere array comprising:

a) contacting a substrate with a surface comprising discrete sites at a density of at least 100 sites per 1 mm², with a solution comprising a population of different particles, wherein said particles do not comprise an optical signature; and

b) applying energy to said substrate or said solution, or both, such that at least a subpopulation of said different particles randomly associate onto sites.

17. (Original) A method according to claim 16 wherein said discrete sites comprise wells.

18. (Original) A method according to claim 16 wherein said energy is in the form of agitation.

19. (Previously presented) A method according to claim 16, wherein said energy is dipping said substrate into said particles.

20. (Previously presented) A method according to claim 19, wherein said substrate is a fiber optic bundle.

21-58. (Cancelled)

59. (Previously presented) A method of determining the presence of a target analyte in a sample comprising:

a) contacting said sample with an array comprising:

i) substrate with a surface comprising discrete sites at a density of at least 100 sites per 1 mm², wherein said sites are wells; and

ii) a population of microspheres randomly distributed on said sites, wherein said population comprises at least a first and a second subpopulation each comprising:

(a) a different bioactive agent; and

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(b) a different identifier binding ligand;

b) determining the presence or absence of said target analyte; and

c) decoding a location of said bioactive agent by correlating said bioactive agent with said location, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to a first and second identifier binding ligands, whereby said first and second identifier binding ligands identify said first and second bioactive agents, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

60. (Currently amended) The method according to claim 45, 46, 52, 55, 58, 59, 66, 67, 68, 69, 70, 71, 72 or 73 59, wherein said first and second bioactive agents are comprise nucleic acids.

61. (Currently amended) The method according to claim 60, wherein said nucleic acids are comprise DNA.

62. (Currently amended) The method according to claim 60, wherein said nucleic acids are comprise single stranded nucleic acids.

63. (Currently amended) The method according to claim 60, wherein said nucleic acids are comprise double stranded nucleic acids.

64. (Currently amended) The method according to claim 45, 46, 52, 55, 58, 59, 66, 67, 68, 69, 70 or 72 59, wherein said first and second bioactive agents are comprise proteins.

65. (Currently amended) The method according to claim 45, 46, 52, 53, 55, 58 or 59 59, wherein said substrate is comprises a fiber optic bundle.

66-74. (Cancelled)

75. (New) The method according to claim 16, wherein said population of different particles comprises at least a first and second subpopulation.

76. (New) The method according to claim 75, wherein said first and second subpopulations each comprise a different bioactive agent.

77. (New) The method according to claim 76, wherein said bioactive agent comprises a protein.

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78. (New) The method according to claim 76, wherein said bioactive agent comprises a nucleic acid.

79. (New) The method according to claim 78, wherein said nucleic acid comprises DNA.

80. (New) The method according to claim 76, wherein said first and second subpopulations of particles each comprise a different identifier binding ligand.

81. (New) The method according to claim 80, wherein said identifier binding ligand comprises a protein.

82. (New) The method according to claim 80, wherein said identifier binding ligand comprises a nucleic acid.

83. (New) The method according to claim 82, wherein said bioactive agent and said identifier binding ligand within the same subpopulation each comprise an identical nucleic acid sequence for binding a decoder binding ligand.

84. (New) The method according to claim 80 further comprising decoding a location of said bioactive agent on said array by correlating said bioactive agent with said location, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to first and second identifier binding ligands, whereby said first and second identifier binding ligands identify said first and second bioactive agents, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

85. (New) The method according to claim 84, wherein said decoder binding ligands comprise proteins.

86. (New) The method according to claim 84, wherein said decoder binding ligands comprise nucleic acids.

87. (New) The method according to claim 16, wherein said substrate comprises a flat planar substrate.

88. (New) The method according to claim 59, wherein said identifier binding ligands comprise proteins.

89. (New) The method according to claim 59, wherein said identifier binding ligands comprise nucleic acids.

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90. (New) The method according to claim 59, wherein comprise decoder binding ligands are proteins.

91. (New) The method according to claim 59, wherein comprise decoder binding ligands are nucleic acids.

92. (New) The method according to claim 59, wherein said substrate comprises a flat planar substrate.

93. (New) A method of determining the presence of a target analyte in a sample comprising:

a) contacting said sample with an array comprising:

i) a substrate with a surface comprising sites at a density of at least 100 sites per 1 mm²; and

ii) a population of particles randomly distributed on said sites, wherein said population comprises at least a first and a second subpopulation each comprising:

(a) a different bioactive agent; and

(b) a different identifier binding ligand;

b) decoding a location of said bioactive agent by correlating said bioactive agent with said location, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to a first and second identifier binding ligands, whereby said first and second identifier binding ligands identify said first and second bioactive agents, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array; and

c) determining the presence or absence of said target analyte.

94. (New) The method according to claim 93, wherein said bioactive agents comprise nucleic acids.

95. (New) The method according to claim 94, wherein said nucleic acids comprise DNA.

96. (New) The method according to claim 94, wherein said nucleic acids comprise single stranded nucleic acids.

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97. (New) The method according to claim 94, wherein said nucleic acids comprise double stranded nucleic acids.

98. (New) The method according to claim 93, wherein said bioactive agents comprise proteins.

99. (New) The method according to claim 93, wherein said identifier binding ligands comprise proteins.

100. (New) The method according to claim 93, wherein said identifier binding ligands comprise nucleic acids.

101. (New) The method according to claim 93, wherein said decoder binding ligands comprise proteins.

102. (New) The method according to claim 93, wherein said decoder binding ligands comprise nucleic acids.

103. (New) The method according to claim 93, wherein said substrate comprises a fiber optic bundle.

104. (New) The method according to claim 93, wherein said substrate comprises a flat planar substrate.

105. (New) The method according to claim 93, wherein said particles are beads.

106. (New) The method according to claim 93, wherein said sites comprise wells.

107. (New) The method according to claim 93, wherein said sites are present in a depression.

108. (New) The method according to claim 107, wherein said sites are contiguous.